

SEQUENCE LISTING

<110> Croteau, Rodney et al.

<120> Transacylases of the Paclitaxel Biosynthetic Pathway

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<150> 09/411,145

<151> 1999-09-30

<160> 58

<170> PatentIn Ver. 2.0

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<213> Taxus cuspidata

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<213> Taxus cuspidata

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      35             40             45

Ser Asn Pro Ser Phe Gln Gln Leu Leu Phe Ser Leu Pro Leu Asp Thr
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Asn Phe Lys Asp Leu Ser Leu Leu Val Val Gln Val Thr Arg Phe Thr
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 115 120 125
 Lys Leu Asp Asp Pro Lys Tyr Leu Gln Phe Phe His Phe Glu Phe Leu
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 Arg Ala Pro Ser Ile Val Glu Lys Ile Val Gln Thr Tyr Phe Ile Ile
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 Asp Leu Glu Thr Ile Asn Tyr Ile Lys Gln Ser Val Met Glu Glu Cys
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 Lys Glu Phe Cys Ser Ser Phe Glu Val Ala Ser Ala Met Thr Trp Ile
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 Gly Tyr Tyr Gly Asn Ser Ile Gly Thr Ala Cys Ala Val Asp Asn Val
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245

250

255

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      35           40           45

Phe Arg Gln Leu Gln Ser Thr Leu Pro Leu Asp Thr Asp Cys Lys Asp
      50           55           60

Leu His Leu Met Thr Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65           70           75           80

Val Met Gly Thr Ser Val His Gln Ser Ile Cys Asp Gly Asn Gly Leu
      85           90           95

Gly Gln Phe Phe Lys Ser Met Ala Glu Met Val Arg Gly Glu Val Lys
      100          105          110

Pro Ser Ile Glu Pro Val Trp Asn Arg Glu Leu Val Lys Pro Glu Asp
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Tyr Ile His Leu Gln Leu Tyr Ile Gly Glu Phe Ile Arg Pro Pro Leu
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165 170 175

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180 185 190

Ala Phe Gln Ile Pro His Asn Glu Asp Val Thr Leu Leu Leu Ala Met
195 200 205

Asp Ala Arg Arg Ser Phe Asp Pro Pro Ile Pro Lys Gly Tyr Tyr Gly
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Asn Val Ile Gly Thr Ala Cys Ala Thr Asn Asn Val His Asn Leu Leu
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Ser Gly Ser Leu Leu His Ala Leu Thr Ile Ile Lys Lys Ser Met Ser
245 250 255

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 Pro Ser Ser Glu Pro Ile Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp
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 Cys Ser Ala Phe Glu Val Val Ser Ala Leu Ala Trp Ile Ala Arg Thr
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attgtagcag cattggtttg gctagcaaag ataaaggctt ttcaaattcc acatagttag 660
aatgtgaagc ttctttttgc aatggacttg aggagatcat ttaatcccc tcttccacat 720
ggatactatg gcaatgcctt tgggtattgca tgtgcaatgg ataatgtcca tgaccttcta 780
agtggatctc ttttgcgcac tataatgatc ataaagaaat caaagttctc tttacacaaa 840
gaactcaact caaaaaccgt gatgagctcg tctgtagtag atgtcaatac gaagtttgaa 900
gatgtagttt caattagtga ttggaggcat tctatatatt atgaagtgga ctttggctgg 960
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<210> 14

<211> 322

<212> PRT

<213> Taxus cuspidata

<400> 14

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Phe Tyr Pro Phe Ala Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu
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Glu Val Glu Cys Thr Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala
          20           25           30

Asp Ser Asp Leu Ser Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser
  35           40           45

Phe Gln Gln Leu Ile Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp
  50           55           60

Leu His Leu Leu Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
  65           70           75           80

Val Val Gly Ala Asn Val Tyr Gly Ser Thr Cys Asp Ala Lys Gly Phe
          85           90           95

Gly Gln Phe Leu Gln Gly Met Ala Glu Met Ala Arg Gly Glu Val Lys
 100           105           110

Pro Ser Ile Glu Pro Ile Trp Asn Lys Arg Thr Gly Glu Ala Arg Arg
 115           120           125

Glu Val Lys Pro Ser Ile Glu Pro Ile Trp Asn Lys Arg Thr Gly Glu
 130           135           140

Ala Arg Arg Leu Tyr Ala Leu Ser Gly Met Ser His Leu Gln Ile Ile
 145           150           155           160

His Ala Pro Val Ile Glu Glu Lys Phe Val Gln Thr Ser Leu Val Ile
          165           170           175

Asn Phe Glu Ile Ile Asn His Ile Arg Arg Arg Ile Met Glu Glu Cys
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180	185	190
Lys Glu Ser Leu Ser Ser Phe Glu Ile Val Ala Ala Leu Val Trp Leu		
195	200	205
Ala Lys Ile Lys Ala Phe Gln Ile Pro His Ser Glu Asn Val Lys Leu		
210	215	220
Leu Phe Ala Met Asp Leu Arg Arg Ser Phe Asn Pro Pro Leu Pro His		
225	230	235
Gly Tyr Tyr Gly Asn Ala Phe Gly Ile Ala Cys Ala Met Asp Asn Val		
245	250	255
His Asp Leu Leu Ser Gly Ser Leu Leu Arg Thr Ile Met Ile Ile Lys		
260	265	270
Lys Ser Lys Phe Ser Leu His Lys Glu Leu Asn Ser Lys Thr Val Met		
275	280	285
Ser Ser Ser Val Val Asp Val Asn Thr Lys Phe Glu Asp Val Val Ser		
290	295	300
Ile Ser Asp Trp Arg His Ser Ile Tyr Tyr Glu Val Asp Phe Gly Trp		
305	310	315
		320

Gly Lys

<210> 15
 <211> 908
 <212> DNA
 <213> Taxus cuspidata

<400> 15
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 gatttggatg ctcataatcc ttcatttcac cagctttctg tttcacctoc agtggattct 180
 gatattgagg gcctccatct tgcagctctt caggtaactc gttttacatg tgggggtttt 240
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 aaaggtgtgg cagagatggt gaggggaaaa gataagccct caattgaacc agtatggaat 360
 agagaaaatg taaagtttga agactataca cgcctccaat tttatcacca tgaattcata 420
 caaccacctt taatagatga gaaaattgtt caaaaatctc ttgttataaa cttggagaca 480
 ataaatatta tcaaacgatg tattatggaa gaatatacaa aatttttctc tacattcgaa 540
 atcgtagcag caatggtttg gctagcaaga acaaaagctt tcaaaattcc acatagtga 600
 aatgcagagc ttctctttac aatggatatg agggatcat ttaatcccc tcttccaaag 660
 ggatactatg gtaatgttat gggtatagta tgtgcattgg ataattgtcaa acacctatta 720
 agtggatcta ttttgctgct tgcaatggtt atacagaaat caagggtttt ctttacagag 780
 aatttcgggt taagatctat gacacaacca tctgcattga ctgtgaagat caagcacaaa 840
 aatgtagttg catgtagtga ttggaggcaa tatggatatg atgaagtgga cttcggctgg 900
 ggtaaacc 908

<210> 16
 <211> 302
 <212> PRT
 <213> Taxus cuspidata

<400> 16
 Phe Tyr Pro Phe Ala Gly Arg Leu Arg Asn Lys Glu Asn Gly Asp Leu
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Glu Val Glu Cys Thr Gly Glu Gly Ala Val Phe Val Glu Ala Met Ala
 20 25 30
 Asp Thr Asp Leu Ser Ser Leu Gly Asp Leu Asp Ala His Asn Pro Ser
 35 40 45
 Phe His Gln Leu Ser Val Ser Pro Pro Val Asp Ser Asp Ile Glu Gly
 50 55 60
 Leu His Leu Ala Ala Leu Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
 65 70 75 80
 Val Leu Gly Val Ser Leu Asn Gln Ser Val Cys Asp Gly Lys Gly Leu
 85 90 95
 Gly Asn Phe Leu Lys Gly Val Ala Glu Met Val Arg Gly Lys Asp Lys
 100 105 110
 Pro Ser Ile Glu Pro Val Trp Asn Arg Glu Met Val Lys Phe Glu Asp
 115 120 125
 Tyr Thr Arg Leu Gln Phe Tyr His His Glu Phe Ile Gln Pro Pro Leu
 130 135 140
 Ile Asp Glu Lys Ile Val Gln Lys Ser Leu Val Ile Asn Leu Glu Thr
 145 150 155 160
 Ile Asn Ile Ile Lys Arg Cys Ile Met Glu Glu Tyr Thr Lys Phe Phe
 165 170 175
 Ser Thr Phe Glu Ile Val Ala Ala Met Val Trp Leu Ala Arg Thr Lys
 180 185 190
 Ala Phe Lys Ile Pro His Ser Glu Asn Ala Glu Leu Leu Phe Thr Met
 195 200 205
 Asp Met Arg Glu Ser Phe Asn Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220
 Asn Val Met Gly Ile Val Cys Ala Leu Asp Asn Val Lys His Leu Leu
 225 230 235 240
 Ser Gly Ser Ile Leu Arg Ala Ala Met Val Ile Gln Lys Ser Arg Phe
 245 250 255
 Phe Phe Thr Glu Asn Phe Arg Leu Arg Ser Met Thr Gln Pro Ser Ala
 260 265 270
 Leu Thr Val Lys Ile Lys His Lys Asn Val Val Ala Cys Ser Asp Trp
 275 280 285
 Arg Gln Tyr Gly Tyr Asp Glu Val Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 17
 <211> 908
 <212> DNA
 <213> *Taxus cuspidata*

<400> 17

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ggtttttgatt accacaatcc agcatttggg aagctacttt actcactacc actggatacc 180
cctatttcacg acctccatcc tctggttgtt caggtaactc gttttacctg cgggggggtt 240
gttgtgggat taagtttgga ccatactata tgtgatggac gtggtgcagg tcaatttctt 300
aaagccctag cagaratggc gaggggagag gctaagccct cattggaacc aatatggaat 360
agagagtgtg tgaagccga agaccttata cgcttgaat tttatcactt tgaatcgatg 420
cgtccacctc caatagttga agaaatggtt caatcatcta ttattataaa tgctgagaca 480
ataagtaata tsaaacaata cattatggaa gaatgtaaag aatcttggtc tgcatttgat 540
gtcgtaggag gattggcttg gctagccagg acaaaggctt ttcaaattcc acatacagag 600
aatgtgatgg ttatttttgc agtggatgcg aggagatcat ttgatccacc acttccaaag 660
ggttactatg gtaatgtcgt tggtaatgca tgtgcattgg ataatgttca agacctotta 720
aatggatctc ttttgcgtag tacaatgatt ataaagaaat caaaggatc tttaaaagag 780
aatataaggg caaaaaactt gacgatacca tctatagtag atgtgaatgt gaaacatgaa 840
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ggsaagcc 908
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<210> 18

<211> 302

<212> PRT

<213> *Taxus cuspidata*

<400> 18

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Phe Tyr Pro Phe Ala Gly Arg Met Arg Asn Lys Gly Asp Gly Glu Leu
  1              5              10              15

Glu Val Asp Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Met Ala
      20              25              30

Asp Asp Asn Leu Ser Val Leu Gly Gly Phe Asp Tyr His Asn Pro Ala
      35              40              45

Phe Gly Lys Leu Leu Tyr Ser Leu Pro Leu Asp Thr Pro Ile His Asp
      50              55              60

Leu His Pro Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65              70              75              80

Val Val Gly Leu Ser Leu Asp His Thr Ile Cys Asp Gly Arg Gly Ala
      85              90              95

Gly Gln Phe Leu Lys Ala Leu Ala Glu Met Ala Arg Gly Glu Ala Lys
      100              105              110

Pro Ser Leu Glu Pro Ile Met Asn Arg Glu Leu Leu Lys Pro Glu Asp
      115              120              125

Leu Ile Arg Leu Gln Phe Tyr His Phe Glu Ser Met Arg Pro Pro Pro
      130              135              140

Ile Val Glu Glu Met Val Gln Ser Ser Ile Ile Ile Asn Ala Glu Thr
      145              150              155              160

Ile Ser Asn Xaa Lys Gln Tyr Ile Met Glu Glu Cys Lys Glu Ser Cys
      165              170              175

Ser Ala Phe Asp Val Val Gly Gly Leu Ala Met Leu Ala Arg Thr Lys
      180              185              190

Ala Phe Gln Ile Pro His Thr Glu Asn Val Met Val Ile Phe Ala Val
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195 200 205

Asp Ala Arg Arg Ser Phe Asp Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
210 -- 215 220

Asn Val Val Gly Asn Ala Cys Ala Leu Asp Asn Val Gln Asp Leu Leu
225 230 235 240

Asn Gly Ser Leu Leu Arg Ala Thr Met Ile Ile Lys Lys Ser Lys Val
245 250 255

Ser Leu Lys Glu Asn Ile Arg Ala Lys Thr Leu Thr Ile Pro Ser Ile
260 265 270

Val Asp Val Asn Val Lys His Glu Asn Ile Val Gly Leu Gly Asp Leu
275 280 285

Arg Arg Leu Gly Phe Asn Glu Val Asp Phe Gly Trp Gly Lys
290 295 300

<210> 19
<211> 911
<212> DNA
<213> *Taxus cuspidata*

<400> 19
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gatctggatg acctcaatcc atcatttcag cagttagttt tttggcatcc attggacact 180
gctattgagg atcttcatct tgtgattgtt caggtaacac gttttacatg tgggggcatt 240
gccgttgagg tgaactttgcc ccatagtgtg tgtgatggac gtggagcacc ccagtttgtt 300
acagcactgg cagaaatggc gaggggagag gttaagccct tattagaacc aatatggaat 360
agagaattgt tgaaccctga agaccctcta catctccagt taaatcaatt tgattcgata 420
tgcccaacct caatgctcga ggaattgggt caagcttctt ttgttataaa tgttgacacc 480
atagaatata tgaacaatg tgttatggag gaatgtaatg atttttgttc gtcctttgaa 540
gtagtggcag cattggtttg gatagcaagg acaaaggctc ttcaaattcc acatactgag 600
aatgtgaagc ttctctttgc gatggatttg aggaaattat ttaatcccc acttccaaat 660
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aattattcga ggtcaagggt agttacaaac ccaaattcat tagatgtgaa caagaaatcc 840
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tggggcaagc c 911

<210> 20
<211> 303
<212> PRT
<213> *Taxus cuspidata*

<400> 20
Tyr Tyr Pro Leu Ala Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu
1 5 10 15
Glu Val Glu Cys Thr Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val
20 25 30
Glu Asp Thr Ile Ser Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser
35 40 45
Phe Gln Gln Leu Val Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp
50 55 60

Leu His Leu Val Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile
 65 70 75 80
 Ala Val Gly Val Thr Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala
 85 90 95
 Pro Gln Phe Val Thr Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys
 100 105 110
 Pro Leu Leu Glu Pro Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp
 115 120 125
 Pro Leu His Leu Gln Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro
 130 135 140
 Met Leu Glu Glu Leu Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr
 145 150 155 160
 Ile Glu Tyr Met Lys Gln Cys Val Met Glu Glu Cys Asn Asp Phe Cys
 165 170 175
 Ser Ser Phe Glu Val Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys
 180 185 190
 Ala Leu Gln Ile Pro His Thr Glu Asn Val Lys Leu Leu Phe Ala Met
 195 200 205
 Asp Leu Arg Lys Leu Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Ile Gly Thr Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu
 225 230 235 240
 Asn Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala
 245 250 255
 Asp Leu Lys Asp Asn Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Asn
 260 265 270
 Ser Leu Asp Val Asn Lys Lys Ser Asn Asn Ile Leu Ala Leu Ser Asp
 275 280 285
 Trp Arg Arg Leu Gly Phe Tyr Glu Ala Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 21
 <211> 911
 <212> DNA
 <213> *Taxus cuspidata*

<400> 21
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 gatctggatg acctcaatcc atcatttcag cagttagttt tttggcatcc attggacact 180
 gctattgagg atcttcatct tgtgattgtt caggtaacac gttttacatg tgggggcatt 240
 gccgttggag tgactttgcc ccatagtgtg tgtgatggac gtggagcacc ccagtttgtt 300
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 agagaattgt tgaaccctga agaccctcta catctccagt taaatcaatt tgattcgata 420
 tgcccacctc caatgctcga ggaattgggt caagcttctt ttgttataaa tgttgacacc 480

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atagaatata tgaacaatg tggtatggag gaatgtaatg atttttgttc gtcctttgaa 540
gtagtggcag cattggtttg gatagcaagg acaaaggctc ttcaaattcc acatactgag 600
aatgtgaagc ttctctttgc gatggatttg aggaaattat ttaatccccc acttccaaat 660
ggatattatg gtaatgccat tggtagtgca tatgcaatgg ataatgtcca agacctctta 720
aatggatctc ttttgcggtgc tataatgatt ataaaaaaag caaaggctga tttaaaagat 780
aattattcga ggtcaagggt agttacaaac ccaaattcat tagatgtgaa caagaaatcc 840
aacaacattc ttgcattgag tgactggagg cggttgggat tttatgaagc cgattttggc 900
tggggcaagc c 911

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<210> 22

<211> 306

<212> PRT

<213> Taxus cuspidata

<400> 22

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Tyr Tyr Pro Leu Ala Gly Arg Leu Glu Thr Cys Asp Gly Met Val Tyr
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Ile Asp Cys Asn Asp Lys Gly Ala Glu Phe Ile Glu Ala Tyr Ala Ser
      20              25              30

Pro Glu Leu Gly Val Ala Glu Ile Met Ala Asp Ser Phe Pro His Gln
      35              40              45

Ile Phe Ala Phe Asn Gly Val Leu Asn Ile Asp Gly His Phe Met Pro
      50              55              60

Leu Leu Ala Val Gln Ala Thr Lys Leu Lys Asp Gly Ile Ala Leu Ala
      65              70              75              80

Ile Thr Val Asn His Ala Val Ala Asp Ala Thr Ser Val Trp His Phe
      85              90              95

Ile Ser Ser Trp Ala Gln Leu Cys Lys Glu Pro Ser Asn Ile Pro Leu
      100             105             110

Leu Pro Leu His Thr Arg Cys Phe Thr Thr Ile Ser Pro Ile Lys Leu
      115             120             125

Asp Ile Gln Tyr Ser Ser Thr Thr Thr Glu Ser Ile Asp Asn Phe Phe
      130             135             140

Pro Pro Pro Leu Thr Glu Lys Ile Phe His Phe Ser Gly Lys Thr Ile
      145             150             155             160

Ser Arg Leu Lys Glu Glu Ala Met Glu Ala Cys Lys Asp Lys Ser Ile
      165             170             175

Ser Ile Ser Ser Phe Gln Ala Leu Cys Gly His Leu Trp Gln Ser Ile
      180             185             190

Thr Arg Ala Arg Gly Leu Ser Pro Ser Glu Pro Thr Thr Ile Lys Ile
      195             200             205

Ala Val Asn Cys Arg Pro Arg Ile Val Pro Pro Leu Pro Asn Ser Tyr
      210             215             220

Phe Gly Asn Ala Val Gln Val Val Asp Val Thr Met Thr Thr Glu Glu
      225             230             235             240

Leu Leu Gly Asn Gly Gly Ala Cys Ala Ala Leu Ile Leu His Gln Lys

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245

250

255

Ile Ser Ala His Gln Asp Thr Gln Ile Arg Ala Glu Leu Asp Lys Pro
 .. 260 265 270

Pro Lys Ile Val His Thr Asn Asn Leu Ile Pro Cys Asn Ile Ile Ala
 275 280 285

Met Ala Gly Ser Pro Arg Phe Pro Ile Tyr Asn Asn Asp Phe Gly Trp
 290 295 300

Gly Lys
 305

<210> 23

<211> 908

<212> DNA

<213> Taxus cuspidata

<400> 23

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 acaggggagg gtgcactgtt tgtggaagcc gtggtggaca atgatctttc agtcttgaaa 120
 gatttggatg cccaaaatgc atcttatgag cagttgotct tttcgcttcc gcccaataca 180
 caggttcagg acctccatcc tctgattctt caggtaactc gttttaaatg tggagggttt 240
 gttgtgggag ttggtttcca ccatagtata tgtgacgcac gaggaggaac tcaatttctt 300
 ctaggcctag cagatatggc aaggggagag actaagcctt tagtggaacc agtatggaat 360
 agagaactga taaaccctga agatcctaag cacctccaat ttcataagtt tggtttgata 420
 cgccaacctc taaaacttga tgaaatttgt caagcatctt ttactataaa ctcaaagata 480
 ataaattaca tcaaacaatg tgttatagaa gaatgtaatg aaattttctc tgcatttgaa 540
 gttgtagtag cattaacttg gatagcaagg acaaaggctt ttcaaattcc acatagttag 600
 aatgtgatga tgctcttttg aatggacgag aggaaatatt ttaatccccc acttccaaag 660
 ggatattatg gtaatgccat tggtaacttc tgtgtaattg aaaatgtaca agacctctta 720
 aatggatctc tttcgcgatc tgtaatgatc acaaagaaat caaagggtccc ttttaattgag 780
 aatttaaggt caagaattgt ggcgaaccaa tctggagtag atgaggaaat taagcatgaa 840
 aacgtagttg gatttggaga ttggaggcga ttgggatttc atgaagtgga cttcggctgg 900
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<210> 24

<211> 302

<212> PRT

<213> Taxus cuspidata

<400> 24

Phe Tyr Pro Phe Ala Gly Arg Ile Arg Gln Lys Glu Asn Glu Glu Leu
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Glu Val Glu Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Val Val
 20 25 30

Asp Asn Asp Leu Ser Val Leu Lys Asp Leu Asp Ala Gln Asn Ala Ser
 35 40 45

Tyr Glu Gln Leu Leu Phe Ser Leu Pro Pro Asn Thr Gln Val Gln Asp
 50 55 60

Leu His Pro Leu Ile Leu Gln Val Thr Arg Phe Lys Cys Gly Gly Phe
 65 70 75 80

Val Val Gly Val Gly Phe His His Ser Ile Cys Asp Ala Arg Gly Gly
 85 90 95

Thr Gln Phe Leu Leu Gly Leu Ala Asp Met Ala Arg Gly Glu Thr Lys
 100 105 110
 Pro Leu Val Glu Pro Val Trp Asn Arg Glu Leu Ile Asn Pro Glu Asp
 115 120 125
 Leu Met His Leu Gln Phe His Lys Phe Gly Leu Ile Arg Gln Pro Leu
 130 135 140
 Lys Leu Asp Glu Ile Cys Gln Ala Ser Phe Thr Ile Asn Ser Lys Ile
 145 150 155 160
 Ile Asn Tyr Ile Lys Gln Cys Val Ile Glu Glu Cys Asn Glu Ile Phe
 165 170 175
 Ser Ala Phe Glu Val Val Val Ala Leu Thr Trp Ile Ala Arg Thr Lys
 180 185 190
 Ala Phe Gln Ile Pro His Ser Glu Asn Val Met Met Leu Phe Gly Met
 195 200 205
 Asp Ala Arg Lys Tyr Phe Asn Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Ile Gly Thr Ser Cys Val Ile Glu Asn Val Gln Asp Leu Leu
 225 230 235 240
 Asn Gly Ser Leu Ser Arg Ala Val Met Ile Thr Lys Lys Ser Lys Val
 245 250 255
 Pro Leu Ile Glu Asn Leu Arg Ser Arg Ile Val Ala Asn Gln Ser Gly
 260 265 270
 Val Asp Glu Glu Ile Lys His Glu Asn Val Val Gly Phe Gly Asp Trp
 275 280 285
 Arg Arg Leu Gly Phe His Glu Val Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 25
 <211> 1320
 <212> DNA
 <213> *Taxus cuspidata*

<400> 25
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 cgagaggctc tctccaaggt gctggtttat tatccccctt ttgctggaag gctgagaaac 240
 acagaaaatg gggatcttga agtggagtgc acaggggagg gtgccgtctt tgtggaagcc 300
 atggcggaca acgaccttc agtattacaa gatttcaatg agtacgatcc atcatttcag 360
 cagctagttt ttaatcttcg agaggatgtc aatattgagg acctccatct tctaactgtt 420
 caggtaaact gttttacatg tggaggattt gttgtgggca caagattcca ccatagtgtg 480
 tctgatggaa aaggaatcgg ccagttactt aaaggcatgg gagagatggc aaggggggag 540
 ttttaagcct cgttagaacc aatatggaat agagaaatgg tgaagcctga agacattatg 600
 tacctccagt ttgatcactt tgatttcata caccacactc ttaatcttga gaagtctatt 660
 caagcatcta tggtaataag ctttgagaga ataaattata tcaaacgatg catgatggaa 720
 gaatgcaaag aatttttttc tgcatttgaa gttgtagtag cattgatttg gctggcaagg 780
 acaaagtctt ttcgaattcc acccaatgag tatgtgaaaa ttatctttcc aatcgacatg 840

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		260						265					270		
Lys	Ile	Ile	Phe	Pro	Ile	Asp	Met	Arg	Asn	Ser	Phe	Asp	Ser	Pro	Leu
	275						280					285			
Pro	Lys	Gly	Tyr	Tyr	Gly	Asn	Ala	Ile	Gly	Asn	Ala	Cys	Ala	Met	Asp
	290					295					300				
Asn	Val	Lys	Asp	Leu	Leu	Asn	Gly	Ser	Leu	Leu	Tyr	Ala	Leu	Met	Leu
305					310					315					320
Ile	Lys	Lys	Ser	Lys	Phe	Ala	Leu	Asn	Glu	Asn	Phe	Lys	Ser	Arg	Ile
			325						330					335	
Leu	Thr	Lys	Pro	Ser	Thr	Leu	Asp	Ala	Asn	Met	Lys	His	Glu	Asn	Val
			340					345					350		
Val	Gly	Cys	Gly	Asp	Trp	Arg	Asn	Leu	Gly	Phe	Tyr	Glu	Ala	Asp	Phe
		355					360					365			
Gly	Trp	Gly	Asn	Ala	Val	Asn	Val	Ser	Pro	Met	Gln	Gln	Gln	Arg	Glu
	370					375					380				
His	Glu	Leu	Ala	Met	Gln	Asn	Tyr	Phe	Leu	Phe	Leu	Arg	Ser	Ala	Lys
385					390					395					400
Asn	Met	Ile	Asp	Gly	Ile	Lys	Ile	Leu	Met	Phe	Met	Pro	Ala	Ser	Met
				405					410					415	
Val	Lys	Pro	Phe	Lys	Ile	Glu	Met	Glu	Val	Thr	Ile	Asn	Lys	Tyr	Val
		420						425					430		
Ala	Lys	Ile	Cys	Asn	Ser	Lys	Leu								
	435						440								

<210> 27
 <211> 1317
 <212> DNA
 <213> Taxus cuspidata

<400> 27
 atggagaaga cagattttaca cgtaaatctg attgagaaag tgatgggttg gccatccccg 60
 cctctgcccc aaaccaccct gcaactctcc tccatagaca acctgccagg ggtaagagga 120
 agcatttttca atgccttggt aattttacaat gcctctccct ctcccaccat gatctctgca 180
 gatcctgcaa aaccaattag agaagctctc gccaaagatcc tggtttatta tccccctttt 240
 gctgggcgcc tcagagagac agaaaatggg gatctggaag tggaatgcac aggggagggt 300
 gctatgtttt tggaagccat ggcagacaat gagctgtctg tgttgggaga ttttgatgac 360
 agcaatccat catttcagca gctacttttt tcgcttcac tcgataccaa tttcaaagac 420
 ctctctcttc tggttgttca ggtaactcgt tttacatgtg gaggctttgt tgttggagt 480
 agtttccacc atggtgtatg tgatggtcga ggagcggccc aattttctaa aggtttggca 540
 gagatggcac ggggagaggt taagctctca ttggaaccaa tatggaatag ggaactagt 600
 aagcttgatg accctaaata ccttcaattt tttcactttg aattcctacg agcgccttca 660
 attgttgaga aaattgttca aacatatttt attatagatt ttgagaccat aaattatatt 720
 aaacaatctg ttatggaaga atgtaaagaa ttttgctctt cattcgaagt tgcacagca 780
 atgacttgga tagcaaggac aagagctttt caaattccag aaagttagta cgtgaaaatt 840
 ctcttcggaa tggacatgag gaactcattt aatccccctc ttccaagcgg atactatggt 900
 aactccattg gtaccgcatg tgcagtggat aatgttcaag acctcttaag tggatctctt 960

```

ttgcgtgcta taatgattat aaagaaatca aaggtctctt taaatgataa tttcaagtca 1020
agagctgtgg tgaagccatc tgaattggat gtgaatatga atcatgaaaa cgtagttgca 1080
tttgctgatt ggagccgatt gggatttgat gaagtggatt ttggttgggg gaatgcggtg 1140
agtgtaaagg ctgtgcaaca acagtctgcg ttagcaatgc aaaattattt tcttttccta 1200
aaaccttcca agaacaagcc cgatggaatc aaaatattaa tgtttctgcc cctatcaaaa 1260
atgaagtcac tcaaaattga aatggaagcc atgatgaaaa aatatgtggc taaagta 1317

```

<210> 28

<211> 439

<212> PRT

<213> Artificial Sequence

<400> 28

```

Met Glu Lys Thr Asp Leu His Val Asn Leu Ile Glu Lys Val Met Val
  1             5             10             15

```

```

Gly Pro Ser Pro Pro Leu Pro Lys Thr Thr Leu Gln Leu Ser Ser Ile
          20             25             30

```

```

Asp Asn Leu Pro Gly Val Arg Gly Ser Ile Phe Asn Ala Leu Leu Ile
          35             40             45

```

```

Tyr Asn Ala Ser Pro Ser Pro Thr Met Ile Ser Ala Asp Pro Ala Lys
          50             55             60

```

```

Pro Ile Arg Glu Ala Leu Ala Lys Ile Leu Val Tyr Tyr Pro Pro Phe
          65             70             75             80

```

```

Ala Gly Arg Leu Arg Glu Thr Glu Asn Gly Asp Leu Glu Val Glu Cys
          85             90             95

```

```

Thr Gly Glu Gly Ala Met Phe Leu Glu Ala Met Ala Asp Asn Glu Leu
          100            105            110

```

```

Ser Val Leu Gly Asp Phe Asp Asp Ser Asn Pro Ser Phe Gln Gln Leu
          115            120            125

```

```

Leu Phe Ser Leu Pro Leu Asp Thr Asn Phe Lys Asp Leu Ser Leu Leu
          130            135            140

```

```

Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val
          145            150            155            160

```

```

Ser Phe His His Gly Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Leu
          165            170            175

```

```

Lys Gly Leu Ala Glu Met Ala Arg Gly Glu Val Lys Leu Ser Leu Glu
          180            185            190

```

```

Pro Ile Trp Asn Arg Glu Leu Val Lys Leu Asp Asp Pro Lys Tyr Leu
          195            200            205

```

```

Gln Phe Phe His Phe Glu Phe Leu Arg Ala Pro Ser Ile Val Glu Lys
          210            215            220

```

```

Ile Val Gln Thr Tyr Phe Ile Ile Asp Phe Glu Thr Ile Asn Tyr Ile
          225            230            235            240

```

```

Lys Gln Ser Val Met Glu Glu Cys Lys Glu Phe Cys Ser Ser Phe Glu
          245            250            255

```

Val Ala Ser Ala Met Thr Trp Ile Ala Arg Thr Arg Ala Phe Gln Ile
 260 265 270
 Pro Glu Ser Glu Tyr Val Lys Ile Leu Phe Gly Met Asp Met Arg Asn
 275 280 285
 Ser Phe Asn Pro Pro Leu Pro Ser Gly Tyr Tyr Gly Asn Ser Ile Gly
 290 295 300
 Thr Ala Cys Ala Val Asp Asn Val Gln Asp Leu Leu Ser Gly Ser Leu
 305 310 315 320
 Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Val Ser Leu Asn Asp
 325 330 335
 Asn Phe Lys Ser Arg Ala Val Val Lys Pro Ser Glu Leu Asp Val Asn
 340 345 350
 Met Asn His Glu Asn Val Val Ala Phe Ala Asp Trp Ser Arg Leu Gly
 355 360 365
 Phe Asp Glu Val Asp Phe Gly Trp Gly Asn Ala Val Ser Val Ser Pro
 370 375 380
 Val Gln Gln Gln Ser Ala Leu Ala Met Gln Asn Tyr Phe Leu Phe Leu
 385 390 395 400
 Lys Pro Ser Lys Asn Lys Pro Asp Gly Ile Lys Ile Leu Met Phe Leu
 405 410 415
 Pro Leu Ser Lys Met Lys Ser Phe Lys Ile Glu Met Glu Ala Met Met
 420 425 430
 Lys Lys Tyr Val Ala Lys Val
 435

<210> 29
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 29
 Thr Thr Leu Gln Leu Ser Ser Ile Asp Asn Leu Pro Gly Val Arg
 1 5 10 15

<210> 30
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 30

Ile Leu Val Tyr Tyr Pro Pro Phe Ala Gly Arg
 1 5 10

<210> 31
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 31
 Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
 1 5 10

<210> 32
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 32
 Lys Gly Leu Ala Glu Ile Ala Arg Gly Glu Val Lys
 1 5 10

<210> 33
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 33
 Asn Leu Pro Asn Asp Thr Asn Pro Ser Ser Gly Tyr Tyr Gly Asn
 1 5 10 15

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 34
 atnctngtnt attatccncc

20

<210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer
 ..
 <400> 35
 tattatccnc cntttgcngg 20
 <210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:PCR primer
 <400> 36
 ttctatccnt tcgcnggnag 20
 <210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:PCR primer
 <400> 37
 tactatccnt tngcnggnag 20
 <210> 38
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:PCR primer
 <400> 38
 ctaaaaccna ccccntttgg 20
 <210> 39
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:consensus
 sequence
 <400> 39
 Phe Tyr Pro Phe Ala Gly Arg
 1 5
 <210> 40
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:consensus

sequence

<400> 40

Tyr Tyr Pro Leu Ala Gly Arg
1 5

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence

<400> 41

Asp Phe Gly Trp Gly Lys Pro
1 5

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 42

cctcatcttt cccccattga taat

24

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 43

aaaaagaaaa taattttgcc atgcaag

27

<210> 44

<211> 1320

<212> DNA

<213> Taxus cuspidata

<400> 44

atggcaggct caacagaatt tgttggaaga agcttagaga gagtgatggt ggctccaagc 60
cagccatcgc ccaaagcttt cctgcagctc tccacccttg acaatctacc aggggtgaga 120
gaaaacattt ttaacacctt gttagtctac aatgcctcag acagagtttc cgtagatcct 180
gcaaaagtaa ttccggcaggc tctctccaag gtgttggtgt actattcccc ttttgcaggg 240
cgtctcagga aaaaagaaaa tggagatctt gaagtggagt gcacagggga ggggtgctctg 300
tttgtggaag ccattggctga cactgacctc tcagtcttag gagatttgga tgactacagt 360
ccttcaacttg agcaactact tttttgtctt ccgcctgata cagatattga ggacatccat 420
cctctgggtgg ttcaggtaac tcgttttaca tgtggagggt ttgttgtagg ggtgagtttc 480
tgccatggta tatgtgatgg actaggagca ggccagtttc ttatagccat gggagagatg 540
gcaaggggag agattaagcc ctctcggag ccaatatgga agagagaatt gctgaagccg 600
gaagaccctt tataccggtt ccagtattat cactttcaat tgatttgccc gccttcaaca 660
ttcgggaaaa tagttcaagg atctcttggt ataacctctg agacaataaa ttgtatcaaa 720

```

caatgcctta gggaagaaaag taaagaattt tgctctgcgt tcgaagttgt atctgcattg 780
gcttgatag caaggacaag ggctcttcaa attccacata gtgagaatgt gaagcttatt 840
tttgcaatgg acatgagaaa attatttaatt ccaccacttt cgaagggata ctacggtaat 900
tttggttgga ccgtatgtgc aatggataat gtcaaggacc tattaagtgg atctcttttg 960
cgtgttgtaa ggattataaa gaaagcaaag gtctctttaa atgagcattt cacgtcaaca 1020
atcgtgacac cccgttctgg atcagatgag agtatcaatt atgaaaacat agttggattt 1080
ggtgatcgaa ggcgattggg atttgatgaa gtagactttg ggtgggggca tgcagataat 1140
gtaagtctcg tgcaacatgg attgaaggat gtttcagtcg tgcaaagtta ttttcttttc 1200
atacgacctc ccaagaataa ccccgatgga atcaagatcc tatcgttcat gccccgtca 1260
atagtgaat ccttcaaatt tgaaatggaa accatgacaa acaaatatgt aactaagcct 1320

```

<210> 45

<211> 440

<212> PRT

<213> *Taxus cuspidata*

<400> 45

```

Met Ala Gly Ser Thr Glu Phe Val Val Arg Ser Leu Glu Arg Val Met
  1                      5                      10                      15

```

```

Val Ala Pro Ser Gln Pro Ser Pro Lys Ala Phe Leu Gln Leu Ser Thr
                20                      25                      30

```

```

Leu Asp Asn Leu Pro Gly Val Arg Glu Asn Ile Phe Asn Thr Leu Leu
                35                      40                      45

```

```

Val Tyr Asn Ala Ser Asp Arg Val Ser Val Asp Pro Ala Lys Val Ile
                50                      55                      60

```

```

Arg Gln Ala Leu Ser Lys Val Leu Val Tyr Tyr Ser Pro Phe Ala Gly
                65                      70                      75                      80

```

```

Arg Leu Arg Lys Lys Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly
                85                      90                      95

```

```

Glu Gly Ala Leu Phe Val Glu Ala Met Ala Asp Thr Asp Leu Ser Val
                100 .                      105                      110

```

```

Leu Gly Asp Leu Asp Asp Tyr Ser Pro Ser Leu Glu Gln Leu Leu Phe
                115                      120                      125

```

```

Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp Ile His Pro Leu Val Val
                130                      135                      140

```

```

Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
                145                      150                      155                      160

```

```

Cys His Gly Ile Cys Asp Gly Leu Gly Ala Gly Gln Phe Leu Ile Ala
                165                      170                      175

```

```

Met Gly Glu Met Ala Arg Gly Glu Ile Lys Pro Ser Ser Glu Pro Ile
                180                      185                      190

```

```

Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp Pro Leu Tyr Arg Phe Gln
                195                      200                      205

```

```

Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro Ser Thr Phe Gly Lys Ile
                210                      215                      220

```

```

Val Gln Gly Ser Leu Val Ile Thr Ser Glu Thr Ile Asn Cys Ile Lys
                225                      230                      235                      240

```

Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe Cys Ser Ala Phe Glu Val
 245 250 255
 Val Ser Ala Leu Ala Trp Ile Ala Arg Thr Arg Ala Leu Gln Ile Pro
 260 265 270
 His Ser Glu Asn Val Lys Leu Ile Phe Ala Met Asp Met Arg Lys Leu
 275 280 285
 Phe Asn Pro Pro Leu Ser Lys Gly Tyr Tyr Gly Asn Phe Val Gly Thr
 290 295 300
 Val Cys Ala Met Asp Asn Val Lys Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320
 Arg Val Val Arg Ile Ile Lys Lys Ala Lys Val Ser Leu Asn Glu His
 325 330 335
 Phe Thr Ser Thr Ile Val Thr Pro Arg Ser Gly Ser Asp Glu Ser Ile
 340 345 350
 Asn Tyr Glu Asn Ile Val Gly Phe Gly Asp Arg Arg Arg Leu Gly Phe
 355 360 365
 Asp Glu Val Asp Phe Gly Trp Gly His Ala Asp Asn Val Ser Leu Val
 370 375 380
 Gln His Gly Leu Lys Asp Val Ser Val Val Gln Ser Tyr Phe Leu Phe
 385 390 395 400
 Ile Arg Pro Pro Lys Asn Asn Pro Asp Gly Ile Lys Ile Leu Ser Phe
 405 410 415
 Met Pro Pro Ser Ile Val Lys Ser Phe Lys Phe Glu Met Glu Thr Met
 420 425 430
 Thr Asn Lys Tyr Val Thr Lys Pro
 435 440

<210> 46

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 46

gggaattcca tatggcaggc tcaacagaat ttgtgg

36

<210> 47

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 47

gtttatacat tgattcggaa ctagatctga tc

32

<210> 48

<211> 6 ..

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 amino acid
motif found in acyl transferases

<220>

<221> VARIANT

<222> (2)..(4)

<223> Any amino acid

<400> 48

His Xaa Xaa Xaa Asp Gly
1 5

<210> 49

<211> 1332

<212> DNA

<213> *Taxus cuspidata*

<400> 49

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atggagaagt ctggttcagc agatctacat gtaaatatca ttgagcgagt ggtgggtggcg 60
ccatgccagc cgacgcccaa aacaatcctg cagctctcta gcattgacaa aatggggagga 120
ggatttgcca acgtattgct agtcttcggg gcctcccatg gcgtttctgc agatcctgca 180
aaaacaattc gagaggctct ctccaagacc ttgggtctttt atttcccttt tgctggggcgg 240
ctcagaaaaga aagaagatgg ggatatcgaa gtggagtgca tagagcaggg agctctgttc 300
gtggaagcca tggcggacaa cgatctttca gtcgtacgag atctggatga gtacaatcca 360
ttatttcggc agctacaatc ttcgctttca ctggatacag attacaagga cctccatctt 420
atgactgttc aggtaaactcc gtttacatgt ggggggttttg tcatgggaac gagtgtacac 480
caaagtatat cggatggaaa tggattgggg caatttttta aaagcatggc agagatagtg 540
aggggagaa g ttaagccctc aatcgaacca atatggaata gagaattggg gaagcctgaa 600
gactatatac acctccagtt gtatgtcagt gaattcattc gccaccttt agtagttgag 660
aaagttgggc aaacatctct tgttataagc ttcgagaaaa taaatcatat caaacgatgc 720
attatggaag aaagtaaaga atctttctct tcatttgaaa ttgtaacagc aatgggttgg 780
ctagcaagga caagggcttt tcaaattcca cacaacgagg atgtgactct tctccttgca 840
atggatgcaa ggagatcatt tgacccccct attccgaagg gatactacgg taatgtcatt 900
ggtactacat atgcaaaaaga taatgtccac aacctcttaa gtggatctct tttgcatgct 960
ctaacagtta taaagaaatc aatgtcctca ttttatgaga atatgacctc aagagtcttg 1020
gtgaacccat ctacattaga tttgagtatg aagtatgaaa atgtagtttc acttagtgat 1080
tggagccggt tgggacataa tgaagtggac tttgggtggg gaaatgcaat aaatgtaagc 1140
actctgcaac aacaatggga aaatgaggta gctataccaa ctttttttac tttccttcaa 1200
actcccaaga atataccaga tggaatcaag atactaatgt tcatgcccc atcaagagag 1260
aaaacattcg aaattgaagt ggaagccatg ataagaaaat atttgactaa agtgtcgcat 1320
tcaaagctat aa 1332
```

<210> 50

<211> 443

<212> PRT

<213> *Taxus cuspidata*

<400> 50

Met Glu Lys Ser Gly Ser Ala Asp Leu His Val Asn Ile Ile Glu Arg
1 5 10 15

Val Val Val Ala Pro Cys Gln Pro Thr Pro Lys Thr Ile Leu Gln Leu

20					25					30						
Ser	Ser	Ile	Asp	Lys	Met	Gly	Gly	Gly	Phe	Ala	Asn	Val	Leu	Leu	Val	
-35					40					45						
Phe	Gly	Ala	Ser	His	Gly	Val	Ser	Ala	Asp	Pro	Ala	Lys	Thr	Ile	Arg	
50					55					60						
Glu	Ala	Leu	Ser	Lys	Thr	Leu	Val	Phe	Tyr	Phe	Pro	Phe	Ala	Gly	Arg	
65					70					75					80	
Leu	Arg	Lys	Lys	Glu	Asp	Gly	Asp	Ile	Glu	Val	Glu	Cys	Ile	Glu	Gln	
85					90					95						
Gly	Ala	Leu	Phe	Val	Glu	Ala	Met	Ala	Asp	Asn	Asp	Leu	Ser	Val	Val	
100					105					110						
Arg	Asp	Leu	Asp	Glu	Tyr	Asn	Pro	Leu	Phe	Arg	Gln	Leu	Gln	Ser	Ser	
115					120					125						
Leu	Ser	Leu	Asp	Thr	Asp	Tyr	Lys	Asp	Leu	His	Leu	Met	Thr	Val	Gln	
130					135					140						
Val	Thr	Pro	Phe	Thr	Cys	Gly	Gly	Phe	Val	Met	Gly	Thr	Ser	Val	His	
145					150					155					160	
Gln	Ser	Ile	Cys	Asp	Gly	Asn	Gly	Leu	Gly	Gln	Phe	Phe	Lys	Ser	Met	
165					170					175						
Ala	Glu	Ile	Val	Arg	Gly	Glu	Val	Lys	Pro	Ser	Ile	Glu	Pro	Ile	Trp	
180					185					190						
Asn	Arg	Glu	Leu	Val	Lys	Pro	Glu	Asp	Tyr	Ile	His	Leu	Gln	Leu	Tyr	
195					200					205						
Val	Ser	Glu	Phe	Ile	Arg	Pro	Pro	Leu	Val	Val	Glu	Lys	Val	Gly	Gln	
210					215					220						
Thr	Ser	Leu	Val	Ile	Ser	Phe	Glu	Lys	Ile	Asn	His	Ile	Lys	Arg	Cys	
225					230					235					240	
Ile	Met	Glu	Glu	Ser	Lys	Glu	Ser	Phe	Ser	Ser	Phe	Glu	Ile	Val	Thr	
245					250					255						
Ala	Met	Val	Trp	Leu	Ala	Arg	Thr	Arg	Ala	Phe	Gln	Ile	Pro	His	Asn	
260					265					270						
Glu	Asp	Val	Thr	Leu	Leu	Leu	Ala	Met	Asp	Ala	Arg	Arg	Ser	Phe	Asp	
275					280					285						
Pro	Pro	Ile	Pro	Lys	Gly	Tyr	Tyr	Gly	Asn	Val	Ile	Gly	Thr	Thr	Tyr	
290					295					300						
Ala	Lys	Asp	Asn	Val	His	Asn	Leu	Leu	Ser	Gly	Ser	Leu	Leu	His	Ala	
305					310					315					320	
Leu	Thr	Val	Ile	Lys	Lys	Ser	Met	Ser	Ser	Phe	Tyr	Glu	Asn	Met	Thr	
325					330					335						
Ser	Arg	Val	Leu	Val	Asn	Pro	Ser	Thr	Leu	Asp	Leu	Ser	Met	Lys	Tyr	
340					345					350						

Glu Asn Val Val Ser Leu Ser Asp Trp Ser Arg Leu Gly His Asn Glu
 355 360 365

Val Asp Phe Gly Trp Gly Asn Ala Ile Asn Val Ser Thr Leu Gln Gln
 370 375 380

Gln Trp Glu Asn Glu Val Ala Ile Pro Thr Phe Phe Thr Phe Leu Gln
 385 390 395 400

Thr Pro Lys Asn Ile Pro Asp Gly Ile Lys Ile Leu Met Phe Met Pro
 405 410 415

Pro Ser Arg Glu Lys Thr Phe Glu Ile Glu Val Glu Ala Met Ile Arg
 420 425 430

Lys Tyr Leu Thr Lys Val Ser His Ser Lys Leu
 435 440

<210> 51
 <211> 1338
 <212> DNA
 <213> *Taxus cuspidata*

<400> 51
 atgaagaaga caggttcggt tgcagagttc catgtgaata tgattgagcg agtcatgggtg 60
 agaccgtgcc tgccttcgcc caaaacaatc ctccctctct cgcgcattga caacatggca 120
 agagcttttt ctaacgtatt gctgggtctac gctgccaaca tggacagagt ctctgcagat 180
 cctgcaaaag tgattcgaga ggctctctcc aagggtgctgg tttattatta cccttttgct 240
 gggcggtcca gaaataaaga aaatggggaa cttgaagtgg agtgcacagg gcagggtgtt 300
 ctgtttctgg aagccatggc tgacagcgac ctttcagtct taacagatct ggataactac 360
 aatccatcgt ttcagcaggt gattttttct ctaccacagg atacagatat tgaggacctc 420
 catctcttga ttgttcaggt aactcgtttt acatgtgggg gttttgttgt gggagcgaat 480
 gtgtatggta gtgcatgcga tgcaaaagga tttggccagt ttcttcaaag tatggcagag 540
 atggcgagag gagaggttaa gccctcgatt gaaccgatat ggaatagaga actggtgaag 600
 ctagaacatt gtatgccctt ccggtatgagt catcttcaaa ttatacatgc acctgtaatt 660
 gaggagaaat ttgttcaaac atctcttggt ataaactttg agataataaa tcatatcaga 720
 cgacgcacatc tggaagaacg caaagaaagt ttatcttcat ttgaaattgt agcagcattg 780
 gtttggctag caaagataaa ggcttttcaa attccacata gtgagaatgt gaagcttctt 840
 tttgcaatgg acttgaggag atcatttaat cccctcttc cacatggata ctatggcaat 900
 gccttttggt ttgcatgtgc aatggataat gtccatgacc ttctaagtgg atctcttttg 960
 cgactataaa tgatcataaa gaaatcaaaag ttctctttac acaaagaact caactcaaaa 1020
 accgtgatga gctcatctgt agtagatgtc aatacgaagt ttgaagatgt agtttcaatt 1080
 agtgattgga ggcattctat atattatgaa gtggactttg ggtggggaga tgcaatgaac 1140
 gtgagcacta tgctacaaca acaggagcac gagaaatctc tgccaactta tttttctttc 1200
 ctacaatcta ctaagaacat gccagatgga atcaagatgc taatgtttat gcctccatca 1260
 aaactgaaaa aattcaaaaat tgaaatagaa gctatgataa aaaaatatgt gactaaagtg 1320
 tgtccgtcaa agttatga 1338

<210> 52
 <211> 445
 <212> PRT
 <213> *Taxus cuspidata*

<400> 52
 Met Lys Lys Thr Gly Ser Phe Ala Glu Phe His Val Asn Met Ile Glu
 1 5 10 15

Arg Val Met Val Arg Pro Cys Leu Pro Ser Pro Lys Thr Ile Leu Pro
 20 25 30

Leu Ser Ala Ile Asp Asn Met Ala Arg Ala Phe Ser Asn Val Leu Leu
 35 40 45
 Val Tyr Ala Ala Asn Met Asp Arg Val Ser Ala Asp Pro Ala Lys Val
 50 55 60
 Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Tyr Pro Phe Ala
 65 70 75 80
 Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95
 Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala Asp Ser Asp Leu Ser
 100 105 110
 Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser Phe Gln Gln Leu Ile
 115 120 125
 Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp Leu His Leu Leu Ile
 130 135 140
 Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Ala Asn
 145 150 155 160
 Val Tyr Gly Ser Ala Cys Asp Ala Lys Gly Phe Gly Gln Phe Leu Gln
 165 170 175
 Ser Met Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Ile Glu Pro
 180 185 190
 Ile Trp Asn Arg Glu Leu Val Lys Leu Glu His Cys Met Pro Phe Arg
 195 200 205
 Met Ser His Leu Gln Ile Ile His Ala Pro Val Ile Glu Glu Lys Phe
 210 215 220
 Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile Ile Asn His Ile Arg
 225 230 235 240
 Arg Arg Ile Met Glu Glu Arg Lys Glu Ser Leu Ser Ser Phe Glu Ile
 245 250 255
 Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys Ala Phe Gln Ile Pro
 260 265 270
 His Ser Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Arg Ser
 275 280 285
 Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly Asn Ala Phe Gly Ile
 290 295 300
 Ala Cys Ala Met Asp Asn Val His Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320
 Arg Thr Ile Met Ile Ile Lys Lys Ser Lys Phe Ser Leu His Lys Glu
 325 330 335
 Leu Asn Ser Lys Thr Val Met Ser Ser Ser Val Val Asp Val Asn Thr
 340 345 350

Lys Phe Glu Asp Val Val Ser Ile Ser Asp Trp Arg His Ser Ile Tyr
 355 360 365
 Tyr Glu Val Asp Phe Gly Trp Gly Asp Ala Met Asn Val Ser Thr Met
 370 375 380
 Leu Gln Gln Gln Glu His Glu Lys Ser Leu Pro Thr Tyr Phe Ser Phe
 385 390 395 400
 Leu Gln Ser Thr Lys Asn Met Pro Asp Gly Ile Lys Met Leu Met Phe
 405 410 415
 Met Pro Pro Ser Lys Leu Lys Lys Phe Lys Ile Glu Ile Glu Ala Met
 420 425 430
 Ile Lys Lys Tyr Val Thr Lys Val Cys Pro Ser Lys Leu
 435 440 445

<210> 53
 <211> 1326
 <212> DNA
 <213> *Taxus cuspidata*

<400> 53
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 ccaagccttc catcgcccaa agctaccgtc cagctctctg tcgttgatag cctaacaatc 120
 tgcaggggaa tttttaacac gttgttggtt ttcaatgccc ctgacaacat ttctgcagat 180
 cctgtaaaaa taattagaga ggctctctcc aaggtgttgg tgtattattt ccctcttgct 240
 gggcggtcca gaagtaaaga aattggggaa cttgaagtgg agtgcacagg ggatgggtgct 300
 ctgtttgtgg aagccatggt ggaagacacc atttcagtct tacgagatct ggatgacctc 360
 aatccatcat ttcagcagtt agtttttttg catccattgg acaactgctat tgaggatctt 420
 catcttgtga ttgttcaggt aacacgtttt acatgtgggg gcattgccgt tggagtgact 480
 ttgccccata gtgtatgtga tggacgtgga gcagcccagt ttgttacagc actggcagag 540
 atggcgaggg gagagggttaa gccctcacta gaaccaatat ggaatagaga attgttgaac 600
 cctgaagacc ctctacatct ccagttaaat caatttgatt cgatatgccc acctccaatg 660
 ctggaggaat tgggtcaagc ttcttttgtt ataaacgttg acaccataga atatatgaag 720
 caatgtgtca tggaggaatg taatgaattt tgttcgtctt ttgaagtagt ggcagcattg 780
 gtttgatag cacggacaaa ggctcttcaa attccacata ctgagaatgt gaagcttctc 840
 tttgcgatgg atttgaggaa attattttaa cccccacttc caaatggata ttatggtaat 900
 gccattggta ctgcatatgc aatggataat gtccaagacc tcttaaattg atctcttttg 960
 cgtgctataa tgattataaa aaaagcaaag gctgatttaa aagataatta ttcgaggtca 1020
 agggtagtta caaaccataa ttcattagat gtgaacaaga aatccgacaa cattcttgca 1080
 ttgagtgact ggaggcgggt gggattttat gaagccgatt ttgggtgggg aggtccactg 1140
 aatgtaagtt ccctgcaacg gttggaaaat ggattgccta tgttttagtac ttttctatac 1200
 ctactacctg ccaaaaacaa gtctgatgga atcaagctgc tactgtcttg tatgccacca 1260
 acaacattga aatcatttaa aattgtaatg gaagctatga tagagaaata tgtaagtaaa 1320
 gtgtga 1326

<210> 54
 <211> 441
 <212> PRT
 <213> *Taxus cuspidata*

<400> 54
 Met Glu Lys Ala Gly Ser Thr Asp Phe His Val Lys Lys Phe Asp Pro
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 Val Met Val Ala Pro Ser Leu Pro Ser Pro Lys Ala Thr Val Gln Leu
 20 25 30

Ser Val Val Asp Ser Leu Thr Ile Cys Arg Gly Ile Phe Asn Thr Leu
 35 40 45
 Leu Val Phe Asn Ala Pro Asp Asn Ile Ser Ala Asp Pro Val Lys Ile
 50 55 60
 Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Phe Pro Leu Ala
 65 70 75 80
 Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95
 Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val Glu Asp Thr Ile Ser
 100 105 110
 Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser Phe Gln Gln Leu Val
 115 120 125
 Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp Leu His Leu Val Ile
 130 135 140
 Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile Ala Val Gly Val Thr
 145 150 155 160
 Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Val Thr
 165 170 175
 Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Leu Glu Pro
 180 185 190
 Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp Pro Leu His Leu Gln
 195 200 205
 Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro Met Leu Glu Glu Leu
 210 215 220
 Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr Ile Glu Tyr Met Lys
 225 230 235 240
 Gln Cys Val Met Glu Glu Cys Asn Glu Phe Cys Ser Ser Phe Glu Val
 245 250 255
 Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys Ala Leu Gln Ile Pro
 260 265 270
 His Thr Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Lys Leu
 275 280 285
 Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly Asn Ala Ile Gly Thr
 290 295 300
 Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu Asn Gly Ser Leu Leu
 305 310 315 320
 Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala Asp Leu Lys Asp Asn
 325 330 335
 Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Tyr Ser Leu Asp Val Asn
 340 345 350
 Lys Lys Ser Asp Asn Ile Leu Ala Leu Ser Asp Trp Arg Arg Leu Gly

355

360

365

Phe Tyr Glu Ala Asp Phe Gly Trp Gly Gly Pro Leu Asn Val Ser Ser
370 -- 375 380

Leu Gln Arg Leu Glu Asn Gly Leu Pro Met Phe Ser Thr Phe Leu Tyr
385 390 395 400

Leu Leu Pro Ala Lys Asn Lys Ser Asp Gly Ile Lys Leu Leu Leu Ser
405 410 415

Cys Met Pro Pro Thr Thr Leu Lys Ser Phe Lys Ile Val Met Glu Ala
420 425 430

Met Ile Glu Lys Tyr Val Ser Lys Val
435 440

<210> 55

<211> 1347

<212> DNA

<213> *Taxus cuspidata*

<400> 55

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gacagactgc cagggatgaa gtttgctact tttagcgccg tgtagtcta caatgccagc 180
tctcaactcca tttttgcaaa tcctgcacag attattcggc aggcctctct caaggtgttg 240
cagtattatc ccgcttttgc cgggcggtgc agacagaaaag aaaatgagga actggaagtg 300
gagtgcacag gggaggggtgc gctgtttgtg gaagccctgg tcgacaatga tctttcagtc 360
ttgcgagatt tggatgcca aaatgcatct tatgagcagt tgctcttttc gcttcgccc 420
aatatacagg ttcaggacct ccctcctctg attcttcagg taactcgttt tacgtgtgga 480
ggttttgttg tgggagtagg ttttcacat ggtatatgag acgcacgagg aggaactcaa 540
tttcttcaag gcctagcaga tatggcaagg ggagagacta agccttttagt ggaaccagta 600
tggaatagag aactgataaa gcccgaaagt ctaatgcacc tccaatttca taagtttggg 660
ttgatacgcc aacctctaaa acttgatgaa atttgcaag catcttttac tataaactca 720
gagataataa attacatcaa acaatgtgtt atagaagaat gtaacgaaat tttctctgca 780
tttgaagttg tagtagcatt aacttgata gcaaggacaa aggccttttca aattccacat 840
aatgagaatg tgatgatgct ctttggaatg gacgcgagga aatattttta tccccactt 900
ccaaagggat attatggtaa tgccattggt acttcatgtg taattgaaa tgtacaagac 960
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attgagaatt taaggtcaag aattgtggcg aaccaatctg gagtagatga ggaaattaag 1080
catgaaaacg tagttggatt tggagattgg aggcgattgg gatttcatga agtggacttc 1140
ggatcgggag atgcagtga catcagcccc atacaacaac gactagagga tgatcaattg 1200
gctatgcgaa attattttct tttccttcga cttacaagg acatgcctaa tggaatcaaa 1260
atactaattg tcatggatcc atcaagagtg aaattattca aagatgaaat ggaagccatg 1320
ataattaaat atatgccgaa agcctaa 1347

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<210> 56

<211> 448

<212> PRT

<213> *Taxus cuspidata*

<400> 56

Met Glu Lys Gly Asn Ala Ser Asp Val Pro Glu Leu His Val Gln Ile
1 5 10 15

Cys Glu Arg Val Met Val Lys Pro Cys Val Pro Ser Pro Ser Pro Asn
20 25 30

Leu Val Leu Gln Leu Ser Ala Val Asp Arg Leu Pro Gly Met Lys Phe

35

40

45

Ala Thr Phe Ser Ala Val Leu Val Tyr Asn Ala Ser Ser His Ser Ile
 50 -- 55 60
 Phe Ala Asn Pro Ala Gln Ile Ile Arg Gln Ala Leu Ser Lys Val Leu
 65 70 75 80
 Gln Tyr Tyr Pro Ala Phe Ala Gly Arg Ile Arg Gln Lys Glu Asn Glu
 85 90 95
 Glu Leu Glu Val Glu Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala
 100 105 110
 Leu Val Asp Asn Asp Leu Ser Val Leu Arg Asp Leu Asp Ala Gln Asn
 115 120 125
 Ala Ser Tyr Glu Gln Leu Leu Phe Ser Leu Pro Pro Asn Ile Gln Val
 130 135 140
 Gln Asp Leu His Pro Leu Ile Leu Gln Val Thr Arg Phe Thr Cys Gly
 145 150 155 160
 Gly Phe Val Val Gly Val Gly Phe His His Gly Ile Cys Asp Ala Arg
 165 170 175
 Gly Gly Thr Gln Phe Leu Gln Gly Leu Ala Asp Met Ala Arg Gly Glu
 180 185 190
 Thr Lys Pro Leu Val Glu Pro Val Trp Asn Arg Glu Leu Ile Lys Pro
 195 200 205
 Glu Asp Leu Met His Leu Gln Phe His Lys Phe Gly Leu Ile Arg Gln
 210 215 220
 Pro Leu Lys Leu Asp Glu Ile Cys Gln Ala Ser Phe Thr Ile Asn Ser
 225 230 235 240
 Glu Ile Ile Asn Tyr Ile Lys Gln Cys Val Ile Glu Glu Cys Asn Glu
 245 250 255
 Ile Phe Ser Ala Phe Glu Val Val Val Ala Leu Thr Trp Ile Ala Arg
 260 265 270
 Thr Lys Ala Phe Gln Ile Pro His Asn Glu Asn Val Met Met Leu Phe
 275 280 285
 Gly Met Asp Ala Arg Lys Tyr Phe Asn Pro Pro Leu Pro Lys Gly Tyr
 290 295 300
 Tyr Gly Asn Ala Ile Gly Thr Ser Cys Val Ile Glu Asn Val Gln Asp
 305 310 315 320
 Leu Leu Asn Gly Ser Leu Ser Arg Ala Val Met Ile Thr Lys Lys Ser
 325 330 335
 Lys Ile Pro Leu Ile Glu Asn Leu Arg Ser Arg Ile Val Ala Asn Gln
 340 345 350
 Ser Gly Val Asp Glu Glu Ile Lys His Glu Asn Val Val Gly Phe Gly
 355 360 365

Asp Trp Arg Arg Leu Gly Phe His Glu Val Asp Phe Gly Ser Gly Asp
 370 375 380
 Ala Val Asn Ile Ser Pro Ile Gln Gln Arg Leu Glu Asp Asp Gln Leu
 385 390 395 400
 Ala Met Arg Asn Tyr Phe Leu Phe Leu Arg Pro Tyr Lys Asp Met Pro
 405 410 415
 Asn Gly Ile Lys Ile Leu Met Phe Met Asp Pro Ser Arg Val Lys Leu
 420 425 430
 Phe Lys Asp Glu Met Glu Ala Met Ile Ile Lys Tyr Met Pro Lys Ala
 435 440 445

<210> 57
 <211> 1317
 <212> DNA
 <213> *Taxus cuspidata*

<400> 57
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 tccaaagaaa ttctccagct ctccagcctc gacaacatac tcagatgtta tgtcagcgta 120
 ttgttcgtct acgacagggt ttcaactgtt tctgcaaatac ctgcaaaaac aattcgagag 180
 gctctctcca aggttttggg ttattattca ccttttgctg gaaggctcag aaacaaagaa 240
 aatggggatc ttgaagtggg gtgcagtggg gaggggtgctg tcttttggtg agccatggcg 300
 gacaacgagc tttcagtcctt acaagatttg gatgagtact gtacatcgct taaacagcta 360
 atttttacag taccaatgga tacgaaaatt gaagacctcc atcttctaag tgttcaggta 420
 actagtttta catgtggggg atttgtttg ggaataagtt tctaccatac tatatgtgat 480
 ggaaaaggac tgggccagtt tcttcaaggc atgagtgaga tttccaaggg agcattttaa 540
 ccctcactag aaccagtatg gaatagagaa atggtgaagc ctgaacacct tatgttcctc 600
 cagttttaata attttgaatt cgtaccacat cctcttaaat ttaagaagat tgttaaagca 660
 tctattgaaa ttaactttga gacaataaat tgtttcaagc aatgcatgat ggaagaatgt 720
 aaagaaaatt tctctacatt tgaaattgta gcagcactga tttggctagc caagacaaag 780
 tctttccaaa ttccagatag tgagaatgtg aaacttatgt ttgcagtcga catgaggaca 840
 tcgtttgacc cccctcttcc aaagggatat tatggtaatg ttattggtat tgcaggtgca 900
 atagataatg tcaaagaact cttaagtggg tcaattttgc gtgctctaata tattatccaa 960
 aagacaatth tctcttttaa agataatthc atatcaagaa gattgatgaa accatctaca 1020
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 tattatgagg cagattgtgg gtgtggaaat ctatcaaata taattcccat ggatcaacaa 1140
 atagagcatg agtcacctgt gcaaagtaga tttatgttgc ttcgatcatc caagaacatg 1200
 caaaatggaa tcaagatact aatgtccatg cctgaatcaa tggcgaaacc attcaaaagt 1260
 gaaatgaaat tcacaataaa aaaatatgtg actggagcgt gtttctctga gttatga 1317

<210> 58
 <211> 438
 <212> PRT
 <213> *Taxus cuspidata*

<400> 58
 Met Glu Lys Leu His Val Asp Ile Ile Glu Arg Val Lys Val Ala Pro
 1 5 10 15
 Cys Leu Pro Ser Ser Lys Glu Ile Leu Gln Leu Ser Ser Leu Asp Asn
 20 25 30

Ile Leu Arg Cys Tyr Val Ser Val Leu Phe Val Tyr Asp Arg Val Ser
 35 40 45
 Thr Val Ser Ala Asn Pro Ala Lys Thr Ile Arg Glu Ala Leu Ser Lys
 50 55 60
 Val Leu Val Tyr Tyr Ser Pro Phe Ala Gly Arg Leu Arg Asn Lys Glu
 65 70 75 80
 Asn Gly Asp Leu Glu Val Glu Cys Ser Gly Glu Gly Ala Val Phe Val
 85 90 95
 Glu Ala Met Ala Asp Asn Glu Leu Ser Val Leu Gln Asp Leu Asp Glu
 100 105 110
 Tyr Cys Thr Ser Leu Lys Gln Leu Ile Phe Thr Val Pro Met Asp Thr
 115 120 125
 Lys Ile Glu Asp Leu His Leu Leu Ser Val Gln Val Thr Ser Phe Thr
 130 135 140
 Cys Gly Gly Phe Val Val Gly Ile Ser Phe Tyr His Thr Ile Cys Asp
 145 150 155 160
 Gly Lys Gly Leu Gly Gln Phe Leu Gln Gly Met Ser Glu Ile Ser Lys
 165 170 175
 Gly Ala Phe Lys Pro Ser Leu Glu Pro Val Trp Asn Arg Glu Met Val
 180 185 190
 Lys Pro Glu His Leu Met Phe Leu Gln Phe Asn Asn Phe Glu Phe Val
 195 200 205
 Pro His Pro Leu Lys Phe Lys Lys Ile Val Lys Ala Ser Ile Glu Ile
 210 215 220
 Asn Phe Glu Thr Ile Asn Cys Phe Lys Gln Cys Met Met Glu Glu Cys
 225 230 235 240
 Lys Glu Asn Phe Ser Thr Phe Glu Ile Val Ala Ala Leu Ile Trp Leu
 245 250 255
 Ala Lys Thr Lys Ser Phe Gln Ile Pro Asp Ser Glu Asn Val Lys Leu
 260 265 270
 Met Phe Ala Val Asp Met Arg Thr Ser Phe Asp Pro Pro Leu Pro Lys
 275 280 285
 Gly Tyr Tyr Gly Asn Val Ile Gly Ile Ala Gly Ala Ile Asp Asn Val
 290 295 300
 Lys Glu Leu Leu Ser Gly Ser Ile Leu Arg Ala Leu Ile Ile Ile Gln
 305 310 315 320
 Lys Thr Ile Phe Ser Leu Lys Asp Asn Phe Ile Ser Arg Arg Leu Met
 325 330 335
 Lys Pro Ser Thr Leu Asp Val Asn Met Lys His Glu Asn Val Val Leu
 340 345 350
 Leu Gly Asp Trp Arg Asn Leu Gly Tyr Tyr Glu Ala Asp Cys Gly Cys

355		360		365
Gly Asn Leu Ser Asn Val	Ile Pro Met Asp Gln Gln	Ile Glu His Glu		
370 --	375	380		
Ser Pro Val Gln Ser Arg	Phe Met Leu Leu Arg	Ser Ser Lys Asn Met		
385	390	395	400	
Gln Asn Gly Ile Lys	Ile Leu Met Ser Met	Pro Glu Ser Met	Ala Lys	
	405	410	415	
Pro Phe Lys Ser Glu Met	Lys Phe Thr Ile Lys	Lys Tyr Val Thr	Gly	
	420	425	430	
Ala Cys Phe Ser Glu Leu				
435				